STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/565,831*
Source: *EFW p*
Date Processed by STIC: *1-30-06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/565,831*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length — The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3_____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4_____Non-ASCII — The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or **Xaa** represents.

10_____Invalid <213> Response — Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220> — Sequence(s) *1-16* missing the <220> "Feature"
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n/Xaa — "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 01/30/2006
PATENT APPLICATION: US/10/565,831   TIME: 16:02:38

Input Set : A:\Q92863 Sequence Listing.txt
Output Set: N:\CRF4\01302006\J565831.raw

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      3 <110> APPLICANT: ONO PHARMACEUTICAL CO., LTD.
      4       Junya TOGUCHIDA
      6 <120> TITLE OF INVENTION: REMEDY FOR CARTILAGE-RELATED DISEASES
      8 <130> FILE REFERENCE: Q92863
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/565,831
C--> 10 <141> CURRENT FILING DATE: 2006-01-25
     10 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/010890
     11 <151> PRIOR FILING DATE: 2004-07-23
     13 <150> PRIOR APPLICATION NUMBER: JP 2003-280191
     14 <151> PRIOR FILING DATE: 2003-07-25
     16 <160> NUMBER OF SEQ ID NOS: 16
     18 <170> SOFTWARE: PatentIn version 3.1
```

Does Not Comply
Corrected Diskette Needed
(Pg. 1-3)

ERRORED SEQUENCES

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     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 36
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Mus musculus
     24 <220> OTHER INFORMATION: Antisence oligonucleotide
     25 <400> SEQUENCE: 1
     26 acagtaccct ggcacctggt gttttattag ccttgg
     28 <210> SEQ ID NO: 2
     29 <211> LENGTH: 36
     30 <212> TYPE: DNA
     31 <213> ORGANISM: Mus musculus
     32 <220> OTHER INFORMATION: Antisence oligonucleotide
     33 <400> SEQUENCE: 2
     34 aaagattgtg aaaggcaagg agcatatggc gaaggt
     36 <210> SEQ ID NO: 3
     37 <211> LENGTH: 36
     38 <212> TYPE: DNA
     39 <213> ORGANISM: Mus musculus
     40 <223> OTHER INFORMATION: Antisence oligonucleotide
     41 <400> SEQUENCE: 3
     42 cagcagataa acccagggat ccaagatctg gttcag
     44 <210> SEQ ID NO: 4
     45 <211> LENGTH: 36
     46 <212> TYPE: DNA
     47 <213> ORGANISM: Mus musculus
     48 <220> OTHER INFORMATION: Antisence oligonucleotide
     49 <400> SEQUENCE: 4
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pls insent (220)
whenever (221),
(222), (223) is
present.

pls insent

Same error

Same error

pls see
item # 36

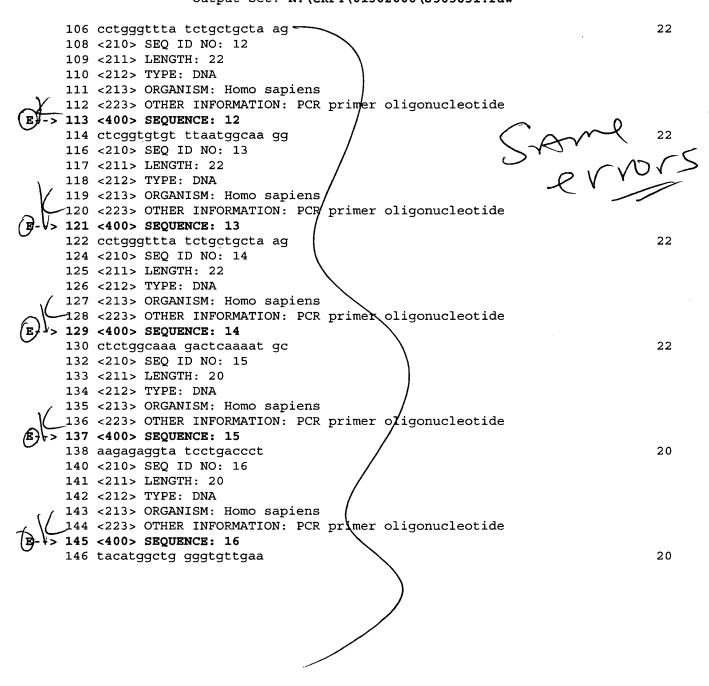```
 50 ggaggagtct gaggtctcgg aaattcgcaa agttct   36
 52 <210> SEQ ID NO: 5
 53 <211> LENGTH: 21
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Homo sapiens
 56 <223> OTHER INFORMATION: PCR primer oligonucleotide
 57 <400> SEQUENCE: 5
 58 acctggtgtt ttattagcct t   21
 60 <210> SEQ ID NO: 6
 61 <211> LENGTH: 21
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Homo sapiens
 64 <223> OTHER INFORMATION: PCR primer oligonucleotide
 65 <400> SEQUENCE: 6
 66 ggccgctgca gggagttaga g   21
 68 <210> SEQ ID NO: 7
 69 <211> LENGTH: 20
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Homo sapiens
 72 <223> OTHER INFORMATION: PCR primer oligonucleotide
 73 <400> SEQUENCE: 7
 74 cgtgtaccta tttcgctttc   20
 76 <210> SEQ ID NO: 8
 77 <211> LENGTH: 20
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Homo sapiens
 80 <223> OTHER INFORMATION: PCR primer oligonucleotide
 81 <400> SEQUENCE: 8
 82 gaggtcccac ttttccttta   20
 84 <210> SEQ ID NO: 9
 85 <211> LENGTH: 21
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Homo sapiens
 88 <223> OTHER INFORMATION: PCR primer oligonucleotide
 89 <400> SEQUENCE: 9
 90 catcgactgg accaccaacg t   21
 92 <210> SEQ ID NO: 10
 93 <211> LENGTH: 21
 94 <212> TYPE: DNA
 95 <213> ORGANISM: Homo sapiens
 96 <223> OTHER INFORMATION: PCR primer oligonucleotide
 97 <400> SEQUENCE: 10
 98 tctcctttaa ctcccgggcg a   21
100 <210> SEQ ID NO: 11
101 <211> LENGTH: 22
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
104 <223> OTHER INFORMATION: PCR primer oligonucleotide
105 <400> SEQUENCE: 11
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*Same errors* [handwritten annotation]

RAW SEQUENCE LISTING                    DATE: 01/30/2006
PATENT APPLICATION:  US/10/565,831      TIME: 16:02:38

          Input Set : A:\Q92863 Sequence Listing.txt
          Output Set: N:\CRF4\01302006\J565831.raw

```
106 cctgggttta tctgctgcta ag                              22
108 <210> SEQ ID NO: 12
109 <211> LENGTH: 22
110 <212> TYPE: DNA
111 <213> ORGANISM: Homo sapiens
112 <223> OTHER INFORMATION: PCR primer oligonucleotide
113 <400> SEQUENCE: 12
114 ctcggtgtgt ttaatggcaa gg                              22
116 <210> SEQ ID NO: 13
117 <211> LENGTH: 22
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
120 <223> OTHER INFORMATION: PCR primer oligonucleotide
121 <400> SEQUENCE: 13
122 cctgggttta tctgctgcta ag                              22
124 <210> SEQ ID NO: 14
125 <211> LENGTH: 22
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
128 <223> OTHER INFORMATION: PCR primer oligonucleotide
129 <400> SEQUENCE: 14
130 ctctggcaaa gactcaaaat gc                              22
132 <210> SEQ ID NO: 15
133 <211> LENGTH: 20
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
136 <223> OTHER INFORMATION: PCR primer oligonucleotide
137 <400> SEQUENCE: 15
138 aagagaggta tcctgaccct                                 20
140 <210> SEQ ID NO: 16
141 <211> LENGTH: 20
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
144 <223> OTHER INFORMATION: PCR primer oligonucleotide
145 <400> SEQUENCE: 16
146 tacatggctg gggtgttgaa                                 20
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Same errors (handwritten annotation)

VERIFICATION SUMMARY   DATE: 01/30/2006
PATENT APPLICATION: **US/10/565,831**   TIME: 16:02:39

Input Set : **A:\Q92863 Sequence Listing.txt**
Output Set: **N:\CRF4\01302006\J565831.raw**

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:1
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:33 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:41 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
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L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:9
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L:105 M:283 W: Missing Blank Line separator, <400> field identifier
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L:121 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:13
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L:129 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:129 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:145 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
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